

Fig. 1 (A)

CAGTGGCAGCAGGCAGTGGCAGCAGGCAGTGGCCCA	36
GGCAGAAATAGCTCCCGCGCGATTCACTGGAGCCTT	72
CCCCGGGCCCCTGGTCCCGGCTACCGGGACTCGCGCG	108
TCCGGATCTCAAAAGCGGCAGAGGCCACCGAAGGGA	144
CAGGAAGCACTTTGGTCCAGACCACACTCCCGGCAC	180
AGTGCGGAAAGAGCCGGCGGGAGCCACTCTGATCCC	216
GGACGCCTCAGCGCCCCCTTGGGCTTGGGCTTGCCC	252
TCGGGCCCAGGGAAGGCTGACCGCGATGCCAGGACGC	288
MetProGlyArg	4
GCTCCCCTCCGCACCGTCCCGGGCGCCCTGGGTGCC	324
AlaProLeuArgThrValProGlyAlaLeuGlyAla	16
TGGCTGCTGGGCGGCCTCTGGGCCTGGACCCTGTGC	360
TrpLeuLeuGlyGlyLeuTrpAlaTrpThrLeuCys	28
GGCCTGTGCAGCCTGGGGGCGGTGGGAGCCCCGCGC	396
GlyLeuCysSerLeuGlyAlaValGlyAlaProArg	40
CCGTGCCAGGCGCCGCAGCAGTGGGAGGGGCGCCAG	432
ProCysGlnAlaProGlnGlnTrpGluGlyArgGln	52
GTTATGTACCAGCAAAGTAGCGGGCGCAACAGCCGC	468
ValMetTyrGlnGlnSerSerGlyArgAsnSerArg	64
GCCCTGCTCTCCTACGACGGGCTCAACCAGCGCGTG	504
AlaLeuLeuSerTyrAspGlyLeuAsnGlnArgVal	76
CGGGTGCTGGACGAGAGGAAGGCGCTGATCCCCTGC	540
ArgValLeuAspGluArgLysAlaLeuIleProCys	88
AAGAGATTATTTGAATATATTTTGCTGTATAAGGAT	576
LysArgLeuPheGluTyrIleLeuLeuTyrLysAsp	100

Fig. 1 (B)

GGAGTGATGTTTCAGATTGACCAAGCCACCAAGCAG	612
GlyValMetPheGlnIleAspGlnAlaThrLysGln	112
TGCTCAAAGATGACCCTGACACAGCCCTGGGATCCT	648
CysSerLysMetThrLeuThrGlnProTrpAspPro	124
CTTGACATTCCTCAAAACTCCACCTTTGAAGACCAG	684
LeuAspIleProGlnAsnSerThrPheGluAspGln	136
TACTCCATCGGGGGGCCTCAGGAGCAGATCACCGTC	720
TyrSerIleGlyGlyProGlnGluGlnIleThrVal	148
CAGGAGTGGTCGGACAGAAAGTCAGCTAGATCCTAT	756
GlnGluTrpSerAspArgLysSerAlaArgSerTyr	160
GAAACCTGGATTGGCATCTATACAGTCAAGGATTGC	792
GluThrTrpIleGlyIleTyrThrValLysAspCys	172
TATCCTGTCCAGGAAACCTTTACCATAAACTACAGT	828
TyrProValGlnGluThrPheThrIleAsnTyrSer	184
GTGATATTGTCTACGCGGTTTTTTTGACATCCAGCTG	864
ValIleLeuSerThrArgPhePheAspIleGlnLeu	196
GGTATTAAAGACCCCTCGGTGTTTACCCCTCCAAGC	900
GlyIleLysAspProSerValPheThrProProSer	208
ACGTGCCAGATGGCCCAACTGGAGAAGATGAGCGAA	936
ThrCysGlnMetAlaGlnLeuGluLysMetSerGlu	220
GACTGCTCCTGGTGAGCCTGTGCATAGGGAAGCGGC	972
AspCysSerTrp***	224
AGCATCGGATGTCAGCCCCCTGCGGCCCCAGCTGGA	1008
GATGGATATGAGACTAGTCAAGATGTGAATGCTAAT	1044
TGGAGAGAAATATAATTTTAGGAAGATGCACATTGA	1080

Fig. 1 (C)

TGTGGGGTTTTGATGTGTCTGATTTTGACTIONACTCAA 1116
 GCTCTGTTTACAGAAGAAAATTGAATGGCGAGGGTG 1152
 TGGCCATATGAACTGACTAGATGGCTAATATGGACA 1188
 CTTTGGGTATTTCTAATGCCTGTTTCAGGGCTGGTTT 1224
 TCTGCATGCACGGGTATACACATAATGCAGTGCCAT 1260
 GCACATAGGGAAGGGTCAGTAAGAGAAGTTTGCCTT 1296
 GGCAGCAAGTATTTATTGTTGACATTATTCAGAATT 1332
 AGTGATAATAAAAAGCAGAGTGATTTTGGTCAATTT 1368
 TATTATTAATTCTTAAATTCCTGACAGAGAATGCCC 1404
 CCTTTATTGCTGCACCGGGTGGGCATTGCTCCAC 1440
 TGAGCCCTACTCCACCCTGTCCCTGCACTCCCTTGG 1476
 TTGCCAAAAAATGATAACTTAAATCCCTTCCAGAC 1512
 TTAAGAATTTTATGGCATGGCCCAATTGATATAAAC 1548
 ATTTAGAAGGAAATGAAAAGCTAAAATAGGAAGTAA 1584
 TTATTCCTCTAAAGAAACATTTTGAGCAAGGCAGTT 1620
 TAGAGAATCCTAATGTCTACACTGGCATAGCACGAG 1656
 CCATGTAAGCTTCTTTTTTTTCTATGCAAGAGTATT 1692
 GATGTATGTGCTGAATCTTCACAGACTTGTCAATAC 1728
 ACAGGCAGTATTCTAAAATAGCACTGAACAGGGAGT 1764
 CAGGAGACTATTGTCTCCTAAACCCAGGACTAGAGT 1800
 TCCCTCGTACTGTCACTCCTTTGGTCATTAAATGCA 1836
 CTGGGCTTGCCCGCACTTTGGCCTTCCTAGAACGCT 1872
 GCTTCATAACCTCTCTGTCTGACTTCTGCATCTCCT 1908
 TCCAGGTCAGCTCATTACAAGAGTTGCTCCCAAGC 1944
 CTGGATGAGTTGCACCTTGCATCTTGAGCATGCATT 1980
 TCTCACAATAATTATTAAGCTGTGTGATAATTTCTG 2016
 CTTTCAGGACACTCATCCATTATCTTGGCTGTGAGC 2052
 TCCTTGGGTACGGGTACCTTGTATGTTTAATTTTAT 2088
 ATCCCTAGCACAAAGCAAGTGCCTGGCACATAGTCA 2124
 GTGCCCTAAGTATTCGTAGAGTGAAGAATGCCAGCC 2160
 TCTCTTGTCCCTGGTTTCCTTATGTGTTGAATGTGG 2196
 TTGAGTTTGTCCATTGCTAGGGAGAGACTTCCAGTA 2232
 ATAAAATTTACTATTCTAGATGCTTCTACTGTTATG 2268

TTTTATCTGCCCATTTATCTTTCTTAGTTACCAGGA	2304
GAAATGTGTGACACCTATATTATAATGAAAACAATC	2340
TTATTACTTATAGTTTATCTATATTAAACAAATTTA	2376
ATTGCATTTTAAAGCATTCTTTGATATTGTTGCTTT	2412
TGCAATAAATATGGATAATCTTGGTTATAAGGGAGT	2448
TAAAACAATGCTGTAATAAATAAAGTGTTTCATGTG	2484
ATCAAAAAAAAAAAAAAAAAAAAAA	2507

Fig. 2 (A)

CCAGACTCGGACCCCCAAGCCGGAAGCCTCTAAAAC	36
AGAAAATTGGAAAATCGGAAAATCAGGAGAGGCCAG	72
GGCTCCTGAGCTGGTCCCAGAGCACATCTTCCACCA	108
GCGCTCAGACAACGCGCGTGACTCTCCACGCCGGG	144
CCTCGGCTCCCTCCCAGGTTTGGCTGACCCGGAGGG	180
CCGCGAATCACGATGCTCACACGCGCTCCCCGCCGC	216
MetLeuThrArgAlaProArgArg	8
CTGGTCCAGGGGCCCCGGGAGACCTGGCTGCTTGGC	252
LeuValGlnGlyProArgGluThrTrpLeuLeuGly	20
GGCCTCTGGGTCTGGATATTGTGCGGCCTGGGGATG	288
GlyLeuTrpValTrpIleLeuCysGlyLeuGlyMet	32
GCGGGCTCCCCGGGAACCCCGCAGCCATGCCAGGCG	324
AlaGlySerProGlyThrProGlnProCysGlnAla	44
CCCCAGCAGTGGGAGGGACGTCAGGTTCTGTACCAG	360
ProGlnGlnTrpGluGlyArgGlnValLeuTyrGln	56
CAGAGCAGCGGGCACAACAGCCGCGCCCTGGTGTCC	396
GlnSerSerGlyHisAsnSerArgAlaLeuValSer	68
TACGATGGTCTCAACCAGCGCGTGCGGGTGCTGGAC	432
TyrAspGlyLeuAsnGlnArgValArgValLeuAsp	80
GAAAGGAAGGCGCTGATCCCCTGCAAGAGATTATTT	468
GluArgLysAlaLeuIleProCysLysArgLeuPhe	92
GAATACATTTTACTCTATAAGGATGGAGTGATGTTT	504
GluTyrIleLeuLeuTyrLysAspGlyValMetPhe	104
CAGATTGAACAAGCCACCAAAGTGTGTGCAAAGATA	540
GlnIleGluGlnAlaThrLysLeuCysAlaLysIle	116

Fig. 2 (B)

CCCTTGGCAGAACCCTGGGATCCTCTCGACATTCCC	576
ProLeuAlaGluProTrpAspProLeuAspIlePro	128
CAGAATTCTACCTTTGAAGATCAGTACTCTATCGGA	612
GlnAsnSerThrPheGluAspGlnTyrSerIleGly	140
GGGCCTCAGGAGCAGATCATGGTCCAGGAATGGTCT	648
GlyProGlnGluGlnIleMetValGlnGluTrpSer	152
GACAGGAGGACAGCCAGATCCTATGAAACCTGGATT	684
AspArgArgThrAlaArgSerTyrGluThrTrpIle	164
GGCGTTTATACAGCCAAGGATTGCTACCCGGTCCAG	720
GlyValTyrThrAlaLysAspCysTyrProValGln	176
GAGACCTTCATTAGGAACTACACTGTGGTCCTGTCC	756
GluThrPheIleArgAsnTyrThrValValLeuSer	188
ACTCGGTTCTTTGATGTGCAGTTGGGCATTAAAGAC	792
ThrArgPhePheAspValGlnLeuGlyIleLysAsp	200
CCCTCTGTGTTACCCCCACCAAGCACGTGCCAGACA	828
ProSerValPheThrProProSerThrCysGlnThr	212
GCACAGCCAGAGAAGATGAAAGAGAACTGCTCCCTG	864
AlaGlnProGluLysMetLysGluAsnCysSerLeu	224
TGAATTTCCATGAGCGGAAGCCACGACCTCAGCTCT	900
***	224
TAGGGACTTTGTGTGGAAATGGACTAGAGGCCAGTT	936
GGAAAGCAACTCGTCACGAGAAGCAAAGCTAGTTTT	972
AGGAAGATAAACCTATGTGGACTTGCTTGTCATCT	1008
GACTGTGGCTGCTCAGCTCTATTTTTTGGAAGGAACC	1044
TGGGTTATCCTTTCTGTGTGCAGGTGTGTAGTCAGT	1080
GCTGTAGGGTAGGACGGGGTGAAGGTGGGGTCGGCA	1116

Fig. 2 (C)

CAAGGAGTTTGCCTCTGCAGAGTGAACCTTTTATTA 1152
 TTGCCAATAAGATTGAAAGTGATAATAAGATATAGT 1188
 ATAATTTTTTTTCAGTTCTCTCCTTACAAAGAAAGTC 1224
 CCTTGCTTGTGTGCACTAGGGTAGTGACAGTTCCCA 1260
 CTGACCCACACCTGCCTCTGGCTACTATGAGATGA 1296
 CCCTTTAAGATTCTTTCCAAGCTTAAATTTTGTCAC 1332
 ATGGCCCACCGGATGTAGATATTCTGCAAGGAAGTA 1368
 GAAACTTGTAATGCAAAGCAATGTTGCCTCTGAAGG 1404
 GAAAAGAAGTTTTAAGCGGGAGGCTTAGACAATCTT 1440
 AGTATCTTCATGTGAGATGAAGTCCGAGCCGTGTGT 1476
 GGTGCTTTGTGTGCAAGAGTACTGACTGCTGTGCTG 1512
 AAACATATGTCTTTTCTAGCGGGCAAACAGGCTTGCA 1548
 AAACAGCACTGAATTGGGAGGCCCCCAAGTAAGGCC 1584
 TAGGATTCTCTGCTACTCTAATCCTTTAAGTAGTAA 1620
 ATGCACTAGGCTAATAGCTCTCGCCTTGCCTTTCTG 1656
 GAAACTCTCTGTCTATATGACTACTGCTCACGCTTC 1692
 CAACATCAGCTCACATGTGCCCCCTGTGAGCTGCTC 1728
 CAATGCCTGAATTCATTGCACCTTACAGCTTGGCAT 1764
 GCCTTGCTCACAATACTCAGTATGCTGCGTGAGGAT 1800
 TTCCTGATTACTGGAACTAACCTCTGTTATCCTGG 1836
 GTAAGAATCCCTTGAGTTACGGGTATCGTGTTCTGT 1872
 TTACTAATATCTCCAGCACCAAGCAAGTGCCTGGCA 1908
 CGTAGTCCGTGCCCCAAACATTTGCAGAGAGGAGCT 1944
 CATCAGCTCTGTGAGTGTTTAGTTTTCTCATCTATT 1980
 AAACAGGGTTGGTTTTTCTGGTTGCTAGGGAGACTT 2016
 GTACTAATGCAACCTACTGTTCTAGATTCTTTATCA 2052
 CCGTGTTTCATTTGACCACGTATCACCTTTTGTTAT 2088
 CAAGAGAAATGTGTGAAGCTTGCTTTATGCTGTAGC 2124
 CATCTATATTGTAATTTATCTCTATAACAATTAAACA 2160
 AATTTATTGACACCCTAAAAAAAAAAAAAAAAAAAAA 2196
 AAAAAA 2202

Fig. 3 (A)

GCAGAGAGCAGGAAAAACAAGCTTTGGTAAGCCTCC	36
GCCAGAGCAGAAAGAGCTGGGGCGATTACGCGGCT	72
TTCCCAGGCCGGTGTCCCGGTGTCCGGAGCCCCCAA	108
GCCAGGAGCCTGTGGAACGGAAAATCGAGAGAGGCC	144
TGAACTGGGTCCCGGAGCACACCTTTCGCCAGGGCG	180
CAGAGAAGGCTCACGCGACTAGTCCAACGCAGGGCC	216
TCGGCTCTCTCTGGAGCTCGGCTGACCCTGGGGCGG	252
CAGATCACGATGCCCCGCGCGCTCCCCGCCGCTG	288
MetProAlaArgAlaProArgArgLeu	9
GTCCAGGGGCCTCGGGGGACCTGGCTGCTGGGAAGC	324
ValGlnGlyProArgGlyThrTrpLeuLeuGlySer	21
CTCTGGGTCTGGGTGCTGTGCGGCCTGGGGATGGCG	360
LeuTrpValTrpValLeuCysGlyLeuGlyMetAla	33
GGCTCCCTGGGAACCCACAGCCATGCCAGGCACCC	396
GlySerLeuGlyThrProGlnProCysGlnAlaPro	45
CAGCAGTGGGAGGGACGCCAGGTTCTGTACCAGCAG	432
GlnGlnTrpGluGlyArgGlnValLeuTyrGlnGln	57
AGCAGCGGGCACAACAACCGCGCCCTGGTGTCTTAC	468
SerSerGlyHisAsnAsnArgAlaLeuValSerTyr	69
GATGGTCTCAACCAGCGCGTGCGGGTGCTGGACGAG	504
AspGlyLeuAsnGlnArgValArgValLeuAspGlu	81
AGGAAAGCGCTGATCCCCTGCAAGAGATTATTTGAA	540
ArgLysAlaLeuIleProCysLysArgLeuPheGlu	93
TACATTTTACTCTATAAGGAGGGAGTGATGTTTCAG	576
TyrIleLeuLeuTyrLysGluGlyValMetPheGln	105

Fig. 3 (B)

ATTGAACAAGCCACCAAACAGTGTGCAAAGATCCCC	612
IleGluGlnAlaThrLysGlnCysAlaLysIlePro	117
TTGGTGAATCCTGGGATCCTCTGGACATTCCCCAG	648
LeuValGluSerTrpAspProLeuAspIleProGln	129
AATTCTACCTTTGAAGATCAGTACTCCATCGGAGGG	684
AsnSerThrPheGluAspGlnTyrSerIleGlyGly	141
CCTCAGGAGCAGATCCTGGTCCAGGAGTGGTCTGAC	720
ProGlnGluGlnIleLeuValGlnGluTrpSerAsp	153
AGAAGAACAGCAAGATCCTATGAAACTTGGATCGGC	756
ArgArgThrAlaArgSerTyrGluThrTrpIleGly	165
GTTTATACAGCCAAGGATTGTTATCCGGTCCAGGAG	792
ValTyrThrAlaLysAspCysTyrProValGlnGlu	177
ACCTTCATCAGGAACCTACACTGTGGTCATGTCCACG	828
ThrPheIleArgAsnTyrThrValValMetSerThr	189
CGGTTCTTTGATGTGCAGCTAGGCATTAAGGACCCC	864
ArgPhePheAspValGlnLeuGlyIleLysAspPro	201
TCTGTGTTCACCCCACCAAGCACATGCCAGGCAGCG	900
SerValPheThrProProSerThrCysGlnAlaAla	213
CAGCCAGAGAAGATGAGTGACGGCTGCTCCTTGTGA	936
GlnProGluLysMetSerAspGlyCysSerLeu***	224
ACTCGCCGAACCTGAACCCAACCTCAGCTCTTAGTGA	972
CCTTGTATGGCAATGGATTAGAGACTAGTTTGAAAG	1008
TAACCTCTTCACTGAAAATAAAGCTAATTTTAGGAAG	1044
ATAAACCCTATGTGGGCTTGCTTGTACATCTGACTG	1080
TGGCTGCTCAGCTCTGTTTTGAGAAGGAAAGGGGCC	1116
ATCCTTTCTGTGAGCAGGTGGGTAGTCAGTGCCATA	1152

Fig. 3 (C)

GAGTAGGAAAGGGCGGGGGTGGGGTCAGCACAAGGA 1188
 GTTTGCCTCTGCAGGGTGAGACTTTTATTATTGCCA 1224
 ATAAGAATCGAAGGTGATAATAAGATATAGAATGCT 1260
 TTTGTTTCAGTTCTCCCCCTTACAAAGAAAGTCCCTTG 1296
 CTTGTCTGCACCAGGGAAGCAAGAGCTCCCAGTGAC 1332
 ACCACCCCCTGCCTCTGGTTACTATAAGATGAGCCT 1368
 TTAAGATTCTTTCTAGACTTAAATTTTGTGCCATGG 1404
 CCCACTGGATGTAGATATTCTACAAGGAAGTAGAAA 1440
 CTTTTAATACGAAGTAATGATTCCTCTAAAGGGAAA 1476
 GGAAGTTTTAAGAGGGAGGCTTGGACAATCTTAGTA 1512
 TTTACACGTGAGATGAAATGAAGAGTCCCGTGTGCT 1548
 GCTCTGTGTGCAAGAGTACTGACCGCTCTGCTGAAC 1584
 CTTTCATGTCTTTTCTAGTGCGGCAACCAGGCTTCCAA 1620
 AATAGCACTGACCTGGGAGGCCCCCAAGTAAGGCCA 1656
 AGAAGTCTCTGCTACTCTAATCTTTTACGTATTAAA 1692
 TGCACTAGGCTAGTAGCCCTTGCCTTTCCTTTCCTG 1728
 AAACCTCTTCAACACAACGTGTGTCTATATGACTACG 1764
 GCTCATGCTTCCAAGGTCAGCTCACATGTGACCTCT 1800
 GTGAGCTGTTCCCTCGCCTGAATTCATTGCATCTTA 1836
 CACCTTGGCATGCCTTGCTCACAATACTCATTATGC 1872
 TGTGTGGGATTTCTCTGATTACTAGAAGCTGACCTCT 1908
 GCTATCCTGGGTAAGAACGCCCTGAGTACGGGTACC 1944
 ATGCTCTGTTTACTTTAGGATCTCCAGCACCAAGCA 1980
 AGTGCCTGGCACATAGTCTGTGCCCTTAACATTTGT 2016
 AGAAAGGAGCTCACCAGCTCTGTCAGTGTTTAGTTT 2052
 CTTTCATCTATTAAACAGGGTTGGTTTTTTCTGGTTGC 2088
 TAGGGAGACTTATAGTAATAACAACCTTACTATTCTAG 2124
 ATTCTTCTTATCGCTGTGTTTTATTTGCCATGTATC 2160
 ATCTTTTGTATATCAAGAGAAGTGTATGATGCTTGCT 2196
 TTATGCCATAGCCATCTATATTGTAATTTATCTATA 2232
 CAATTAAACAAATTTAATGAACCCTATGAATTATTC 2268
 TTTGATGTGTTTGTGTTTTTGTAAAGAAATATGGAGGAA 2304
 CTGAATTATAAAGAAAATAAAATCCTTCTGTAATAA 2340

Fig. 3 (D)

TCAAATAAAGTACTTCCCATAATCAAAACCAAAAAA 2376

AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2403

Fig. 4

(1)	1	10	20	30	40	50	50
(2)	1						50
(3)	1						50
(1)	51	60	70	80	90	100	100
(2)	51						100
(3)	51						100
(1)	101	110	120	130	140	150	150
(2)	101						150
(3)	101						150
(1)	151	160	170	180	190	200	200
(2)	151						200
(3)	151						200
(1)	201	210	220	230	240	250	250
(2)	201						250
(3)	201						250

Fig. 5

(1)	1	10	20	30	40	50
(2)	1	MPGRAPLRIV	PGALGAWLLG	GLWAWLEGGI	CSLGAVGAPR	PCQAPQOWEG
		MLTRAPRRLV	QGPRETWLLG	GLWVWLEGGI	GMA GSPGT PQ	PCQAPQOWEG
(1)	51	60	70	80	90	100
(2)	51	ROVMYQQSSG	RNSRAILLSYD	GENORVRVLD	ERKALTPCKR	LEEXYLLLYKD
		ROVLYQQSSG	HNSRAELVSYD	GENORVRVLD	ERKALTPCKR	LEEXYLLLYKD
(1)	101	110	120	130	140	150
(2)	101	GVMFOEDQAT	KQGSKMTETQ	PWDRLEDPON	STFEEDQYSIG	GPOEQITVQE
		GVMFOEDQAT	KLCAKIPIAE	PWDRLEDPON	STFEEDQYSIG	GPOEQITVQE
(1)	151	160	170	180	190	200
(2)	151	WSDRKSARSY	ELWIGIMLVK	DCYPAVOEHIT	INYSVITSTR	RFDIOLGCHK
		WSDRRTARSY	ELWIGVYIAK	DCYPAVOEHIT	RNYTVITSTR	RFDVOTGCHK
(1)	201	210	220	230	240	250
(2)	201	PSVHTLPPSTG	QMAQLERMSH	DGSW*		
		PSVHTLPPSTG	QTAQPEKMKH	NCSL*		

Fig. 6

(kb)		
9.46	↑	Heart
7.46	↑	Brain
4.40	↑	Placenta
2.37	↑	Lung
1.35	↑	Liver
		Skeletal Muscle
		Kidney
		Pancreas
		Spleen
		Thymus
		Prostate
		Testis
		Ovary
		Small Intestine
		Colon
		Peripheral Blood
		Fetal Brain
		Fetal Lung
		Fetal Liver
		Fetal Kidney

9.46

7.46

4.40

2.37

1.35

Fig. 7

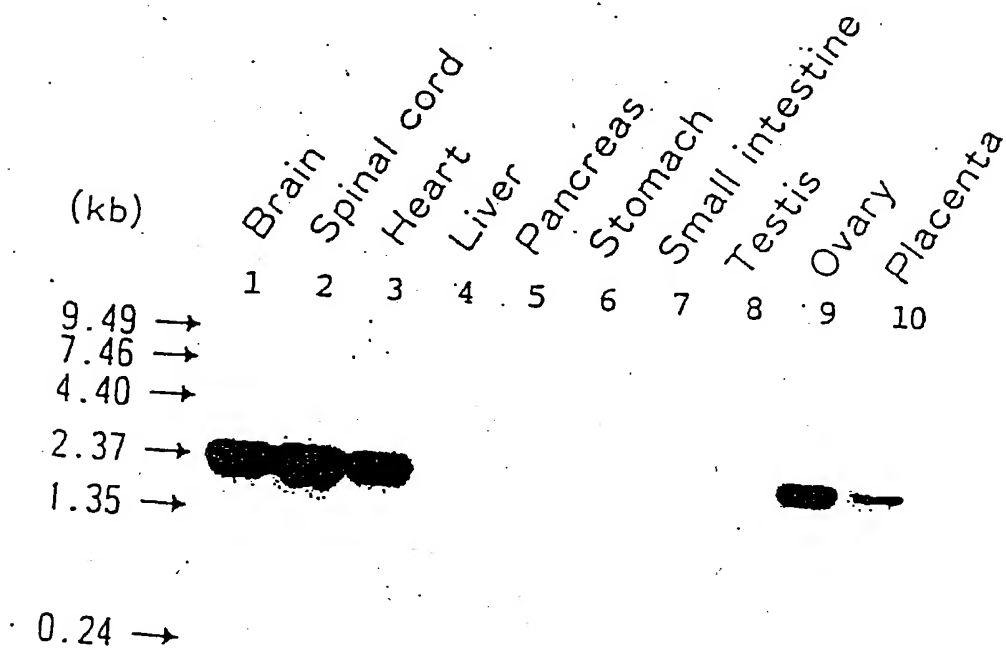


Fig. 8

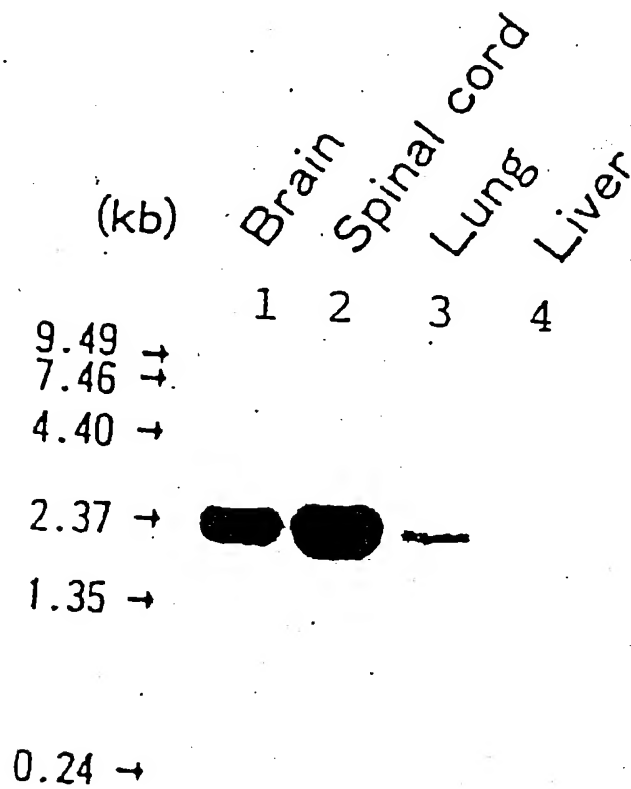


Fig. 9

